-SWA1 SEQUENCE PROTOCOL <110> Degussa AG <120> New nucleotide sequences which codes for the luxS gene 5 <130> 00\0457 BT <140> 10 <141> <160> 4 <170> PatentI Ver. 2.1 15 <210> 1 <211> 1902 <212> DNA <213> Corynebacterium glutamicum 20 <220> <221> CDS <222> (342)..(1610) <223> luxS gene 25 <400> 1 ggtaggagta aaaaacgcag $\sqrt{gagggcgtcg}$  aaaagcgttc gtctgtgccg taacccgtga 60 cgcgctggcc gttggtatcg  $\dot{q}$ cgacccagt cggtgcccag gtaggggcat gcggtttgtg 120 30 cggtgcgttc gaccgcgggc atcgcgtcga tgggaaggcc gtcagtaatt acttccgggg 180 ctgcctcggt ggtggtctct ggggtttgctt caggttccgc cggggtacaa gcggtgagca 240 tgatggaagc agcgaggata gtaggtaatg tacgacgcat gcagtcaagc ctagatcgtg 300 35 tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356 Met Lys Lys Gly Asn 40 caa ccg ggc gcg atg agc tat cgc ac agt atc cac att ttg aca gcc 404 Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala tcg ctg ctg gtc gtg ggg ttg gga gct\tcc gcc cgc ctg acg ctg ccg Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro 452 45 atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr 500 50 45 40 548 ttc tat gga tca acc aaa cgc gta gat ttg agd cac ggc atg cag ctg Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu 55 55 ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att tt $\hbar$  atg gtg ccg atc 596 Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Wet Val Pro Ile

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} ]	_	gtg Val	ccc Pro	gtg Val	tcc Ser	att Ile 90	tat Tyr	ctg Leu	ctg Leu	ttc Phe	ccg Pro 95	ctg Leu	ttt Phe	ttc Phe	ctc Leu	tat Tyr 100	cta Leu	644
	5	cag Gln	gtg Val	atg Met	cct Pro 105	gac Asp	gtg Val	aga Arg	ggc Gly	att Ile 110	att Ile	gcg Ala	att Ile	ttg Leu	ggt Gly 115	gcg Ala	aca Thr	692
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	45	aaa Lys	acc Thr	tcc Ser	ttg Leu 265	Glu	gca Ala	gca Ala	ctt Leu	cac His 270	Arg	gtc Val	aca Thr	gaa Glu	ccg Pro 275	ttg Leu	ttg Leu	1172
	50	ggt Gly	att Ile	aat Asn 280	Phe	gtg Val	att Ile	tct Ser	gtc Val 285	Asp	ggt Gly	gat Asp	\gtt Val	cgc Arg 290	Gln	ctg Leu	ccc Pro	1220
	55	atg Met	aaa Lys 295	Thr	gaa Glu	gcc Ala	acc Thr	ctt Leu 300	Leu	cga Arg	att Ile	gct Ala	caa Gln 305	Gly	gcg Ala	atc Ile	gga Gly	1268

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WAI		aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr 310 325	
	5	tac gaa gaa gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly 330 335 340	
	1/0	ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile 345 350 355	
	15	ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val 360 365 370	
		ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg  Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu  375  380  1508	
	20	ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp 390 405	
	25	tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac  Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp  410  415  420	
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	35	gcattttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720 gtgctgcttg ctgatgacca cgaaattgtg aggctcggac tccgagctgt gctggaaagc 1780 gccgaggaca ttgaagtggt gggcgaagtc tccaccgccg aaggtgcggt gcaggcagcc 1840	
	40	caagaaggcg gaatcgacgt catcttgat gacctccgat tcggccccgg cgtccaagga 1900 ac 1902	
	45	<210> 2 <211> 423 <212> PRT <213> Corynebacterium glutamicum	
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		His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala 20 25 30	
	55	Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val 35 40 45	
		Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser	

His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Aro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu 5 Phe Phe Leu Tyn Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala 10 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gl $lac{1}{\lambda}$  Val Met Gly Pro Val Val Ser Ala Ile Val Thr 15 135 Val Ala Ile Asp Tyr Åla Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Ash Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala 20 170 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala 25 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met 200 Leu Leu His Val Ser Glu Gln 🖟 Glu Ile Leu Val Ala Glu Met Glu Glu ВO 215 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln 35 250 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val 265 40 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala 45 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val\ Arg Leu Asp Val Val 50 330 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala 55 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu 360 355

Cyll A 1

Leu His G  $\stackrel{\hbox{\scriptsize Ala}}{\longrightarrow}$  Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala 370 380

Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala 385 390 395 400

Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu 415

Ser Ser Pro Thr Asp Asp Glu

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<212> DNA

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<223> Primer luxS-int1

<400> 3

tcgtgaccgt ggctattgat

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